



FIGURE 1 (1/2)

| | | | |
|-----------------|---------------|---|-----|
| (SEQ ID NO: 9) | {CAA69226} | 1 | 50 |
| (SEQ ID NO: 2) | {PRSS11-Like} | MQIPRAALLP LLLLLLAAPA SAQLSRAGRS APLAAGCPDR CEPARCPPQP | |
| (SEQ ID NO: 10) | {AAB94569} | ----- | |
| Consensus | | -----MAAPRAGRG AGWSLRAWRA LGGIRWGRRP | |
| | | ----- | |
| | | 51 | 100 |
| | {CAA69226} | EHCEGGRARD ACGCCEVCGA PEGAACGLQE GPCGEGLCV VPFGVPASAT | |
| | {PRSS11-Like} | ----- | |
| | {AAB94569} | RLTPDLRALL TSGTSD...P RARVTYGTGS LWARLSVGVT EPRACLTSGT | |
| | Consensus | ----- | |
| | | 101 | 150 |
| | {CAA69226} | VRRRAQAGLC VCASSEPVCG SDANTYANLC QLRAASRRSE RLHRPPVIVL | |
| | {PRSS11-Like} | ----- | |
| | {AAB94569} | PGPRAQLTAV TPDTRTREAS ENSGTRSRAW LAVALGAGGA VLLLLWGGGR | |
| | Consensus | ----- | |
| | | 151 | 200 |
| | {CAA69226} | ORGACGQQQE D..PNSLRHK YNFIADVVEK IAPAVVHIEL FRKLPPFSKRE | |
| | {PRSS11-Like} | ALPA.SAGLH Q..LSSPRYK FNFIADVVEK IAPAVVHIEL FLRHPLFGRN | |
| | {AAB94569} | GPPAVLAAMP SPPPASPRSQ YNFIADVVEK TAPAVVYIEI LDRHPFLGRE | |
| | Consensus | ---A-----S-R-- -NFIADVVEK -APAVV-IE- ----P---R- | |
| | | 201 | 250 |
| | | * | |
| | {CAA69226} | VPVASGSGFI VSEDGLIVTN AHVVTN.... ..KHRVKVEL KNGATYEAKI | |
| | {PRSS11-Like} | VPLSSGSGFI MSEAGLIITN AHVVSSNSAA PGRQQLKVQL QNGDSYEATI | |
| | {AAB94569} | VPISNGSGFV VAADGLIVTN AHVVAD.... ..RRRVVRVL LSGDTYEAVV | |
| | Consensus | VP---GSGF- ----GLI-TN AHVV-----V-L --G--YEA-- | |

FIGURE 1 (2/2)

| | | | |
|---------------|-------------|------------------------|------------------------|
| | 251 | * | 300 |
| {CAA69226} | KDVDEKADIA | LIKIDHQGKL PVLLLGSRSE | LRPGEFVVAI GSPFSLQNTV |
| {PRSS11-Like} | KDIDKKS DIA | TIKIHPKKL PVLLLGHSAD | LRPGEFVVAI GSPFALQNTV |
| {AAB94569} | TAVDPVADIA | TLRIQTKEPL PTLPLGRSAD | VRQGEFVVAM GSPFALQNTI |
| Consensus | ---D---DIA | ---I-----L P-L-LG-S--- | -R-GEFVVA- GSPF-LQNT- |
| | 301 | * | 350 |
| {CAA69226} | TTGIVSTTQR | GGKELGLRNS DMDYIQTDAI | INYGNSSGGPL VNLDGEVIGI |
| {PRSS11-Like} | TTGIVSTAQR | EGRELGLRDS DMDYIQTDAI | INYGNSSGGPL VNLDGEVIGI |
| {AAB94569} | TSGIVSSAQR | PARDLGLPQT NVEYIQTDAI | IDFGNSSGGPL VNLDGEVIGV |
| Consensus | T-GIVS--QR | ----LGL--- ---YIQTDA- | I--GNSGGPL VNLDGEVIG- |
| | 351 | | 400 |
| {CAA69226} | NTLKVTAGIS | FAIPSDKIKK FLTESHDR.Q | AKGKAITKKK YIGIRMSLT |
| {PRSS11-Like} | NTLKVTAGIS | FAIPSDRITR FLTEFQDK.Q | IKD...WKKR FIGIRMRTIT |
| {AAB94569} | NTMKVTAGIS | FAIPSDRLRE FLHRGEKKNS | SSGISGSQRR YIGVMMLTSL |
| Consensus | NT-KVTAGIS | FAIPSD---- FL----- | ----- -IG--M---- |
| | 401 | | 450 |
| {CAA69226} | SSKAKELKDR | HRDFPDVISG AYIIEVIPDT | PAEAGGLKEN DVIISINGQS |
| {PRSS11-Like} | PSLVDELKAS | NPDFPEVSSG IYVQEVAPNS | PSQGGIQDG DIIVKVNGRP |
| {AAB94569} | PSILAEQLR | EPSFPDVQHG VLIHKVILGS | PAHRAGLRPG DVILAIGEQM |
| Consensus | -S---EL--- | ---FP-V--G -----V---- | P----G---- D-I----- |
| | 451 | | 489 |
| {CAA69226} | VVSANDVSDV | IKRESTLMV VRRGNEDIMI | TVIPERIDP |
| {PRSS11-Like} | LVDSSSELQEA | VLTESPLLE VRRGNDDLLE | SIAPEVVM- |
| {AAB94569} | VQNAEDVYEA | VRTQSQLAVQ IRRGRETLTL | YVTPEVTE- |
| Consensus | ----- | ----S-L--- -RRG----- | ---PE---- |

FIGURE 2 (1/1)

HtrA3 (BC034390) (SEQ ID NO: 11) x PRSS11-Like (SEQ ID NO: 2)

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101 CALQAASRRALQLSGTPVRQLQKGACP..LGLHQLSSPRYKFNFIAADVVE 148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   1 .....MHLALPASAGLHQLSSPRYKFNFIAADVVE 29

149 KIAPAVVHIELFLRHPLFGRNVPLSSGSGFIMSEAGLIITNAHVVSNSA 198
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   30 KIAPAVVHIELFLRHPLFGRNVPLSSGSGFIMSEAGLIITNAHVVSNSA 79

199 APGRQQLKVQLONGDSYEATIKDIDKKS DIATI KIH PKKKL PVLLLGHSA 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   80 APGRQQLKVQLONGDSYEATIKDIDKKS DIATI KIH PKKKL PVLLLGHSA 129

249 DLRPGEFVVAIGSPFALQNTVTGTGIVSTA QREGRELGLRDSMDYIQTDA 298
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  130 DLRPGEFVVAIGSPFALQNTVTGTGIVSTA QREGRELGLRDSMDYIQTDA 179

299 IINYGNSSGGPLVNLDGEVIGINTLKVTAGISFAIPSDRITRFLTEFQDKQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  180 IINYGNSSGGPLVNLDGEVIGINTLKVTAGISFAIPSDRITRFLTEFQDKQ 229

349 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVVSSGIYVQE VAPN SPSQ 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  230 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVVSSGIYVQE VAPN SPSQ 279

399 RGGIQDGDIIVKVNGRPLVDSSELQEAVLTESPLLLEVRRGNDLLFSIA 448
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  280 RGGIQDGDIIVKVNGRPLVDSSELQEAVLTESPLLLEVRRGNDLLFSIA 329

449 PEVVM 453
      | | | |
  330 PEVVM 334

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FIGURE 4

A. Unique HtrA3 Long Form Exons

| | | | | |
|-----------------|--|-----------|----|-----------------|
| | E1 589-bp | 12,083-bp | E2 | |
| (SEQ ID NO: 12) | GCGCCTGCCCCGTTGGgtaagcgctcggggg... ..ttcccgccagcgagGTCTCCACCAGCTGA | | | (SEQ ID NO: 13) |
| | E2 100-bp | 4,024-bp | E3 | |
| (SEQ ID NO: 14) | AGAGCTCTTCTGAGgtgggtgaatacccc... ..tctccctggctgcagACACCCGCTGTTTGG | | | (SEQ ID NO: 15) |

B. Unique PRSS11-Like Exon

| | | | | |
|-----------------|---|----------|----|-----------------|
| | E1 1,138-bp | 4,024-bp | E2 | |
| (SEQ ID NO: 16) | AGAGCTCTTCTGAGgtgggtgaatacccc... ..tctccctggctgcagACACCCGCTGTTTGG | | | (SEQ ID NO: 17) |

C. Common HtrA3 Long form and PRSS11-Like Exons

| | | | | |
|-----------------|--|-----------|---------------|-----------------|
| (SEQ ID NO: 18) | E3/E2 223-bp | 4,586-bp | E4/E3 | (SEQ ID NO: 19) |
| | AAGATCCATCCCAAGgtgggtgggcgtggg... ..ccttctctctcctagAAAAAGCTCCCTGTG | | | |
| SEQ ID NO: 20) | E4/E3 195-bp | 756-bp | E5/E4 | (SEQ ID NO: 21) |
| | GATGCCATCATCAACgtgagtgcccaggac... ..ttcctccccttgagTACGGGAAGTCCGGG | | | |
| (SEQ ID NO: 22) | E5/E4 33-bp | 1,733-bp | E6/E5 | (SEQ ID NO: 23) |
| | CCACTGGTGAACCTGgtaagtgtcccctag... ..tacctccctgcccagGATGGCGAGGTCATT | | | |
| (SEQ ID NO: 24) | E6/E5 115-bp | 90,643-bp | E7/E6 | (SEQ ID NO: 25) |
| | ACAAGCAGATCAAAGgtaaagagctcacct... ..gtgtttcatttccagACTGGAAGAAGCGCT | | | |
| (SEQ ID NO: 26) | E7/E6 49-bp | 1,672-bp | E8/E7 | (SEQ ID NO: 27) |
| | GACGATCACACCAAGgtgagtgctgaaga... ..gcagactctttccagCCTGGTGGATGAGCT | | | |
| (SEQ ID NO: 28) | E8/E7 96-bp | 1,691-bp | E9/E8 1140-bp | (SEQ ID NO: 29) |
| | TTCACCTTCTCAGAGgtaggctctgccaga... ..ctctcctgttggcagAGGCGGCATCCAAGA | | | |

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